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(54) Primers and probes for hepatitis C detection

(57) The invention provides oligonucleotide probes for detecting hepatitis C virus nucleic acids from the U.S., Japan, and HCV-C prototype strains, as well as oligonucleotide primers for amplifying such nucleic acids. The invention also provides methods and kits for amplifying and detecting said nucleic acids. The amplification methods preferably include the reverse transcription of the viral genomic RNA to create cDNA and the subsequent amplification of the cDNA by the polymerase chain reaction. Oligonucleotide probes can then be used to detect the presence of amplified DNA by hybridization.

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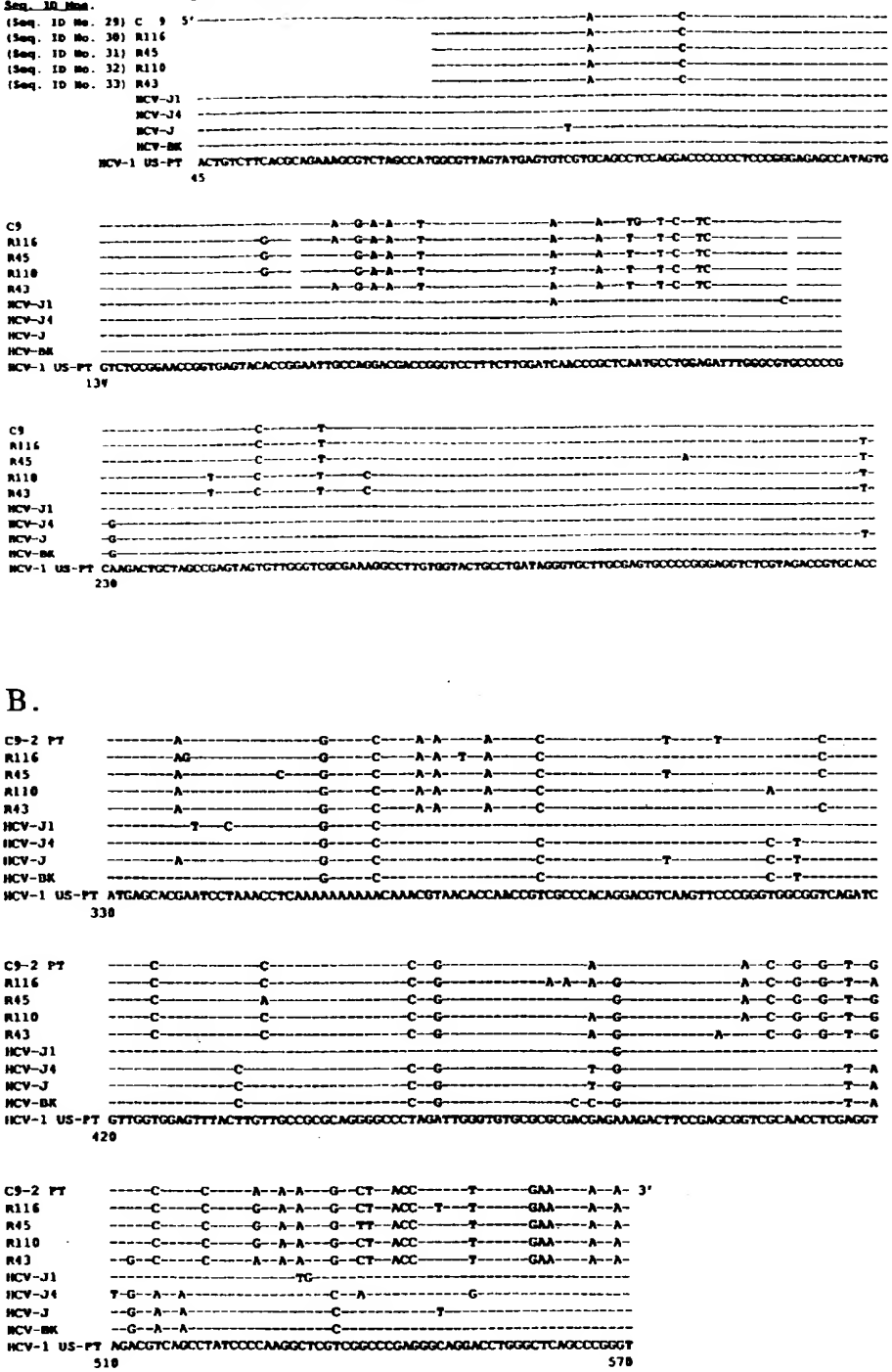
Figure 1

A.

Alignment of 5' Untranslated Region and Contiguous Open Reading Frame of C9 Variant With Additional Isolates Prototype HCV Sequences



B.

Description

The present invention provides improved primers and probes for the detection of Hepatitis C virus, a causative agent of non-A, non-B hepatitis. The reagents include particular oligonucleotide primers for both reverse transcription of the viral RNA genome and subsequent amplification by the polymerase chain reaction of the cDNA so produced. Sequence specific oligonucleotide probes are provided for the detection of amplified HCV nucleic acid sequences. The primers and probes are useful in a diagnostic test for the detection of HCV infection. This diagnostic test has important applications in both clinical and epidemiological settings.

Hepatitis C virus (HCV) is one of an unknown number of agents responsible for non-A, non-B hepatitis (NANBH). The prototypical HCV was identified from a cDNA clone of a blood-borne NANBH virus obtained from the plasma of an infected chimpanzee as reported in Choo et al., 1989, Science 244:359-362. Nucleotide sequences of genes from this prototype HCV are described in European Patent Publication Nos. 318,216; 388,232; and 398,748. The nucleotide sequence of the HCV genome was reported and compared to related virus in Choo et al., 1991, Proc. Natl. Acad. Sci. USA 88:2451-2455.

Sequences from other strains have since been reported. The genome of HCV exhibits a large degree of nucleic acid sequence heterogeneity between isolates. The isolation of cDNA from the HCV RNA genome was reported in Kuboet al., 1989, Nuc. Acids Res. 17:10367-10372. The authors constructed a reverse transcription primer based on the sequence reported in Choo et al., 1989, supra. The fragment of the HCV genome isolated showed 79.8% homology with the prototype HCV sequence. Sequences from three different regions obtained by a similar protocol were reported in Takeuchi et al., 1990, Gene 91:287-291. Sequence homology with the prototype sequence was reported as low as 73.5% for one of the regions.

The HCV genomic sequence from a strain isolated from Japanese patients was reported in Kato et al., 1990, Proc. Natl. Acad. Sci. USA 87:9524-9528. The sequence showed 77.4% homology with the prototype HCV genome over the region compared. A sequence for the entire coding region of the HCV genome reported in Takamizawa et al., 1991, J. Virol. 65(3):1105-1113 showed 77% homology with the prototype HCV strain.

In Japan, two main strains, designated strains K1 and K2, have been observed based on a 400 nucleotide region of the genome. These strains have sequence homology with the prototype HCV sequence as low as 67% (see Enomoto et al., 1990, Biochem. Biophys. Res. Commun. 170(3):1021-1025). The K2 strain could be further subdivided into two groups, designated Ka and Kb, with about 20% nucleotide variation between the groups and about 5% nucleotide variation within each group.

Similar levels of homology with the prototype HCV sequence were reported in Kato et al., 1990, J. Clin. Invest. 86:1764-1767. From 15 patients, cDNA segments were amplified and sequenced The amplified portion, 37 nucleotides corresponding to positions 3525-3561 in the prototype sequence, showed 68-78% homology with the prototype HCV sequence.

HCV genomic RNA can be detected in sera by creating cDNA from the genomic RNA, amplifying the cDNA with the polymerase chain reaction, and subsequently probing with sequence-specific oligonucleotides. Because of the sequence heterogeneity among HCV strains, primers and probes are likely to be strain-specific, unless a region in which the sequence is conserved across strains can be found. One such conserved region is at the 5'-end of the HCV genome.

The 5'-terminal noncoding sequence of the HCV genome was first reported in Okamoto et al., 1990, Japan J. Exp. Med. 60(3):167-177. Comparison between two strains suggested that the 5'-terminal noncoding sequence is conserve. The conserved nature of the 5'-terminal noncoding sequence of the HCV genome was also reported in Han et al., 1991, Proc. Natl. Acad. Sci. USA 88:1711-1715. Partial sequences of a 341 nucleotide region obtained from 11 HCV isolates collected from individuals from five continents were compared. Seven sequences showed complete homology with the prototype sequence; the remaining four showed between one and five base mismatches.

In Okamoto et al., 1990, Japan J. Exp. Med. 60(3):215-222, primers for various regions of the HCV genome, including the conserved 5' noncoding region were described. The primers selected from conserved regions successfully amplified nucleic acid from most of the strains tested; primers chosen from heterogeneous regions amplified nucleic acid from a smaller subset of strains. However, the amplification efficiency with these primers was low. The reference describes a two-stage PCR amplification; the second round of amplification was performed on the previously amplified target region using a second set of primers nested within the region amplified by the first set of primers.

A PCR amplification requiring two rounds of amplification using two sets of primers was also reported in Garson et al., 1990, Lancet 335:1419-1422. A region encoding a nonstructural protein (NS5) was amplified. Due to sequence heterogeneity, there are HCV sequences not recognized by these primers (see Garson et al., 1990, Lancet 336:878-879). Consequently, primers in the conserved 5' noncoding region were tried, but to obtain sufficient sensitivity, a two-sage amplification using sets of nested primers was still necessary. Amplification of the 5'-terminal region using a two-stage amplification with nested primers was also reported in Kanai et al., 1990, Lancet 336:245.

Amplification using two rounds of amplification with nested primers is not only inefficient but also greatly increases the probability of contamination. The problems of contamination are well known in the art; opening the reaction tube to

change primers and add reagents between amplification steps is best avoided if at all possible. The contamination problem is further aggravated by the need to change reaction conditions between the initial reverse transcription step and the subsequent PCR amplification.

There is still a need for primer oligonucleotides for amplifying HCV sequences, each chosen from a conserved region so that all, or almost all, strains will be amplified, and amplification methods efficient enough that amplification with one set of primers is sufficient. There is also a need for probe oligonucleotides for the detection of the amplified cDNA chosen from a conserved region in between the two conserved regions to which the primers hybridize. Reaction protocol and reagents are needed that allow reverse transcription and PCR to occur using the same reagents, thereby eliminating the need to open the reaction tube during the amplification process.

Moreover, ten percent of NANBH cases are nonreactive with the prototype capsid and envelope antigens, see Chaudhary et al., 1991, J. Clinical Microbiology 29:2329-2330 and Hosein et al., 1991, PNAS 8:3647-3651. Thus, the development of PCR based diagnostics and antigens encoded by new isolates will improve the dependability of serologically based diagnostic tests. The present invention meets these needs by providing primers, probes, and methods for detecting HCV.

The specific primers and sequence specific oligonucleotide probes provided can be used in a homogeneous reverse transcription-polymerase chain reaction (RT-PCR) that enables amplification and detection of the viral RNA genomic sequences. The efficiency of amplification using the primers and methods of the present invention eliminates the need for a second round of PCR amplification with nested primers, and the high sensitivity of the resulting test provides reliable detection of the nucleic acid.

One aspect of the invention relates to specific oligonucleotide primers. The invention provides compositions comprising an oligonucleotide primer for amplifying an HCV nucleic acid wherein said primer is suitable for amplifying a nucleic acid subsequence from an HCV strain or isotype selected from the group consisting of Japan, US and C9 strains. The primers provided function both in the reverse-transcription of the viral RNA genome and the subsequent amplification of the cDNA produced using the polymerase chain reaction. The primers hybridize to sequences from conserved regions of the HCV genome and, therefore, bind to a variety of strains. The efficiency of amplification using the provided primers is sufficient to eliminate the need for a second round of PCR amplification with nested primers.

Another aspect of the invention relates to probes capable of detecting the presence of HCV genomic nucleic acid regardless of the strain. The probes are complementary to regions conserved across strains. Diagnostic tests using the probes of the present invention can detect a large number of HCV strains without compromising specificity. Thus, the invention provides compositions comprising an oligonucleotide probe for detecting the presence of Hepatitis C virus nucleic acids, wherein the probe is suitable for detecting the nucleic acid of an HCV strain or variant strain selected from the group consisting of Japan, US, and C9 prototype strains.

A third aspect of the invention relates to kits. These kits take a variety of forms and can comprise one or more reverse-transcription, amplification, or detection reagents, e.g., primers, probes, polymerases, glycosylases, buffers, and nucleoside triphosphates.

Another aspect of the invention relates to methods for amplifying and detecting HCV RNA.

European Patent Application No. 92114115.6 (EP-A-529 493) provides a kit for the detection of nucleic acid specific to a C9 isolate of hepatitis virus, the kit comprising a compartment which contains a nucleic acid probe which binds substantially to a nucleic acid subsequence of the HCV-C9 virus.

In addition, European Patent Application No. 92114115.6 provides compositions comprising a viral nucleic acid sequence substantially homologous to SEQ ID. NO. 28. A cDNA clone, pHCV-C9, containing such a viral sequence, termed here the C9 isolate, is deposited with the American Type Culture Collection and has Deposit No. 75265

European Patent Application No. 92114115.6 also provides oligonucleotide probes and primers for detecting a nucleic acid sequence specific to the C9 isolate and related variants. The probes of the invention preferably comprise a subsequence selected from the following group:

SEQ ID NO. 33 5'-TTGCCGGAAAGACTGGGTCCTTTC-3' (nt174-197)
SEQ ID NO. 34 5'-CAAAAGAAACACAAACCGCCGCCC-3' (nt374-397)
SEQ ID NO. 35 5'-CCAGCCCATCCCGAAAGATCGGCG-3' (nt527-550)
SEQ ID NO. 36 (MY160) 5'-TGTCCGGTCATTTGGGCG-3' (nt216-233)

European Patent Application No. 92114115.6 further provides oligonucleotide primers for the amplification of nucleic acid sequences specific to a C9 isolate. Primers of the invention for specifically amplifying the C9 variant and related isolates preferably comprise a nucleic acid sequence selected from the following group of upstream primers:

SEQ ID NO. 37 5'-AAACCCACTCTATGTCCGGTC-3' (nt204-224);
SEQ ID NO. 38 5'-GTACGCCGGAATTGCCGGAAA-3' (nt163-183); and
SEQ ID NO. 39 5'-CCTCAAAGAAAAACCAAAAGA-3' (nt360-380);

for use with one of the following downstream primers:

SEQ ID NO. 40 5'-TGGCGTCTCCCACGCGGCTGG-3' (nt509-529); and
SEQ ID NO. 41 5'-CTTTCCCCAGGACCTGCCGGT-3' (nt555-575).

European Patent Application No. 92114115.6 also provides probes which substantially bind sequences of the C9 isolate and previously identified Hepatitis C isolates. Preferred probes of this category include:

SEQ ID NO. 42 KY150 5'- CATAGTGGTCTGCGGAACCGGTGAGT - 3'.

The present invention provides probes for detecting non-C9 HCV sequences. More specifically the present invention provides a process for detecting the presence of Hepatitis C genomic nucleic acid, wherein said Hepatitis C genomic nucleic acid is selected from the group consisting of Japan, U.S., and C9 prototype stains, comprising: (a) amplifying a subsequence of the nucleic acid; (b) mixing the amplified nucleic acid with an oligonucleotide probe specific to the subsequence under conditions wherein the probe binds to the subsequence to form a stable hybrid duplex; and (c) detecting hybrids formed between the subsequence and the probe.

The method may further comprise, before step (a), the step of amplifying a subsequence of the sequence specific to the virus. Amplification is preferably achieved by the use the polymerase chain reaction method. The primers and probes above are preferably used in the methods of the invention.

To aid in understanding the invention, several terms are defined below.

"Amplification reaction mixture" refers to an aqueous solution comprising the various reagents used to amplify a target nucleic acid. These include: enzymes, aqueous buffers, salts, target nucleic acid, and deoxynucleoside triphosphates. Depending upon the context, the mixture can be either a complete or incomplete amplification reaction mixture.

"Amplification reaction system" refers to any *in vitro* means for multiplying the copies of a target sequence of nucleic acid. Such methods include, but are not limited to, polymerase chain reaction amplification (PCR), DNA ligase, QB RNA replicase, and RNA transcription-based amplification systems. These involve multiple amplification reagents and are more fully described below.

"Amplification reaction tube(s)" refers to a container suitable for holding the amplification reagents. Generally, the tube is constructed of inert components so as to not inhibit or interfere with the amplification system being used. Where the system requires thermal cycling of repeated heating and cooling, the tube must be able to withstand the cycling process and, typically, precisely fit the wells of the thermocycler.

"Amplification reagents" refer to the various buffers, enzymes, primers, deoxynucleoside triphosphates (both conventional and unconventional), and primers used to perform the selected amplification procedure.

"Amplifying" or "Amplification", which typically refers to an "exponential" increase in target nucleic acid, is being used herein to describe both linear and exponential increases in the numbers of a select target sequence of nucleic acid.

"Bind(s) substantially" refers to complementary hybridization between an oligonucleotide and a target sequence and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired priming for the PCR polymerases or detection of hybridization signal.

The phrase "biologically pure" refers to material that is substantially or essentially free from components which normally accompany it as found in its native state. For instance, affinity purified antibodies or monoclonal antibodies exist in a biologically purified state.

"Hybridizing" refers the binding of two single stranded nucleic acids via complementary base pairing.

"Nucleic acid" refers to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, would encompass known analogs of natural nucleotides that can function in a similar manner as naturally occurring nucleotides.

"Nucleotide polymerases" refers to enzymes able to catalyse the synthesis of DNA or RNA from nucleoside triphosphate precursors. In the amplification reactions of this invention, the polymerases are template-dependent and typically add nucleotides to the 3'-end of the polymer being formed. It is most preferred that the polymerase is thermostable as described in U.S. Patent Nos. 4,889,818 and 5,079,352.

The term "oligonucleotide" refers to a molecule comprised of two or more deoxyribonucleotides or ribonucleotides, such as primers, probes, nucleic acid fragments to be detected, and nucleic acid controls. The exact size of an oligonucleotide depends on many factors and the ultimate function or use of the oligonucleotide. Oligonucleotides can be prepared by any suitable method, including, for example, cloning and restriction of appropriate sequences and direct chemical synthesis by a method such as the phosphotriester method of Narang et al., 1979, Meth. Enzymol. 68:90-99; the phosphodiester method of Brown et al, 1979, Meth. Enzymol. 68:109-151; the diethylphosphoramidite method of Beaucage et al., 1981, Tetrahedron Lett. 22:1859-1862; and the solid support method of U.S. Patent No. 4,458,066.

The term "primer" refers to an oligonucleotide, whether natural or synthetic, capable of acting as a point of initiation of DNA synthesis under conditions in which synthesis of a primer extension product complementary to a nucleic acid

strand is induced, i.e., in the presence of four different nucleoside triphosphates and an agent for polymerization (i.e., DNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. A primer is preferably a single-stranded oligodeoxyribonucleotide. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 15 to 25 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template but must be sufficiently complementary to hybridize with a template.

In the disclosed embodiments of the invention, sequence specific primers and probes are provided. It will be apparent to those of skill in the art that, provided with those embodiments, additional sequence specific primers and probes can be prepared by, for example, the addition of nucleotides to either the 5' or 3' ends, which nucleotides are complementary to the target sequence or are uncomplementary to the target sequence. So long as primer compositions serve as a point of initiation for extension on the target sequences, and so long as the primers and probes comprise at least 14 consecutive nucleotides contained within those exemplified embodiments, such compositions are within the scope of the invention.

The term "primer" may refer to more than one primer, particularly in the case where there is some ambiguity in the information regarding one or both ends of the target region to be amplified. For instance, if a region shows significant levels of polymorphism in a population, mixtures of primers can be prepared that will amplify alternate sequences. A primer can be labeled, if desired, by incorporating a label detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (as commonly used in an ELISA), biotin, or haptens and proteins for which antisera or monoclonal antibodies are available. A label can also be used to "capture" the primer, so as to facilitate the immobilization of either the primer or a primer extension product, such as amplified DNA, on a solid support.

"Probe" refers to an oligonucleotide which binds through complementary base pairing to a subsequence of a target nucleic acid. It will be understood by one of skill in the art that probes will typically substantially bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labelled as with isotopes or indirectly labelled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the target.

"Recombinant" when referring to a nucleic acid probe refers to an oligonucleotide which is free of native proteins and nucleic acid typically associated with probes isolated from the cell, which naturally contains the probe sequence as a part of its native genome. Recombinant probes include those made by amplification means such as PCR and genetic cloning methods where bacteria are transformed with the recombinant probe.

The term "reverse transcriptase" refers to an enzyme that catalyzes the polymerization of deoxyribonucleoside triphosphates to form primer extension products that are complementary to a ribonucleic acid template. The enzyme initiates synthesis at the 3'-end of the primer and proceeds toward the 5'-end of the template until synthesis terminates. Examples of suitable polymerizing agents that convert the RNA target sequence into a complementary, copy-DNA (cDNA) sequence are avian myeloblastosis virus reverse transcriptase and Thermus thermophilus DNA polymerase, a thermostable DNA polymerase with reverse transcriptase activity.

The terms "sequence-specific oligonucleotide" and "SSO" refer to oligonucleotides that have a sequence, called a "hybridizing region," exactly complementary to the sequence to be detected, typically sequences characteristic of a particular allele or variant, which under "sequence-specific, stringent hybridization conditions" will hybridize only to that exact complementary target sequence. Relaxing the stringency of the hybridizing conditions will allow sequence mismatches to be tolerated; the degree of mismatch tolerated can be controlled by suitable adjustment of the hybridization conditions. Depending on the sequences being analyzed, one or more sequence-specific oligonucleotides may be employed. The terms "probe" and "SSO probe" are used interchangeably with SSO.

A "sequence specific to" a particular viral isolate is a sequence unique to the isolate, that is, not shared by other previously characterized isolates. A probe containing a subsequence complementary to a sequence specific to an isolate will typically not hybridize to the corresponding portion of the genome of other isolates under stringent conditions (e.g., washing the solid support in 2xSSC, 0.1% SDS at 70°C).

An antigen or epitope specific to a particular isolate is one that is unique to the isolate and is not shared by other previously characterized isolates. An immunoglobulin raised against the antigen or epitope will not cross react with antigens on previously characterized isolates in standard assays, such as ELISA.

The term "substantially identical" indicates that two or more nucleotide sequences share a majority of their sequence. Generally, this will be at least about 90% of their sequence and preferably about 95% of their sequence. Another indication that sequences are substantially identical is if they hybridize to the same nucleotide sequence under stringent conditions (see, e.g., Sambrook et al., Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1985). Stringent conditions are sequence-dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent con-

ditions will be those in which the salt concentration is at least about 0.2 molar at pH 7 and the temperature is at least about 60°C.

"Subsequence" refers to a sequence of nucleic acids that comprise a part of a longer sequence of nucleic acids.

The term "target region" refers to a region of a nucleic acid to be analyzed and can include a polymorphic region.

The term "thermostable polymerase enzyme" refers to an enzyme that is relatively stable to heat and catalyzes the polymerization of nucleoside triphosphates to form primer extension products that are complementary to one of the nucleic acid strands of the target sequence. The enzyme initiates synthesis at the 3'-end of the primer and proceeds toward the 5'-end of the template until synthesis terminates. A purified thermostable polymerase enzyme is described more fully in U.S. Patent No. 4,889,818.

Figure 1 provides an alignment of the novel variant HCV sequence C9, four related variants, and the prototype Japan and U.S. HCV isolates.

The Hepatitis C virus is a small RNA virus containing a single, positive sense, molecule of RNA about 10,000 nucleotides in length. The genome contains a single, long, open reading frame believed to be translated into a single, large polyprotein and subsequently processed. The open reading frame begins at nucleotide 343 (using the numbering system from the prototype virus) following an untranslated region (UTR). The 5'UTR sequence is relatively conserved and may be important in viral replication and regulation. The 5'-end of the coding region is also conserved. Certain primers and probes of the present invention hybridize to the conserved region at the 5'-end of the HCV genome.

The oligonucleotide sequences of the hybridizing regions of the primers and probes of the invention are presented below. Those skilled in the art will realize that an oligonucleotide sequence used as the hybridizing region of a primer can also be used as the hybridizing region of a probe. Suitability of a primer sequence for use as a probe depends on the hybridization characteristics of the primer. Similarly, an oligonucleotide used as a probe can be used as a primer.

The oligonucleotides shown in Table 1 are positive sense (upstream) primers or probes. The listing is in order based on the position of the 3'-end of the oligonucleotide when hybridized to genomic nucleic acid. The oligonucleotides that hybridize closest to the 5'-end of the genome are listed first.

Table 1

Oligo	Sequence Listing	Sequence	Position (nt)
KY65	SEQ ID NO: 1	5'-CCAAGCTTCACCATAGATCACT	16-29
KY79	SEQ ID NO: 2	5'-GGCGACACTCCACCATAGATCACT	6-29
KY98	SEQ ID NO: 3	5'-CCAAGCTTAGATCACTCCCCTGTGAGGAACT	21-44
KY96	SEQ ID NO: 4	5'-CCAAGCTTCACGCAGAAAGCGTCTAGCCAT	50-74
KY80	SEQ ID NO: 5	5'-GCAGAAAGCGTCTAGCCATGGCGT	56-79
KY144	SEQ ID NO: 6	5'-ACGCAGAAAGCGTCTAGCCATGGCGT	54-79
KY83	SEQ ID NO: 7	5'-CCTCCAGGACCCCCCCTCCCGGGAGAGCCA	99-128
KY84	SEQ ID NO: 8	5'-GAGTACACCGGAATTGCCAGGACGACC	149-175
KY85	SEQ ID NO: 9	5'-ACCCGCTCAATGCCTGGAGAT	194-214
KY67	SEQ ID NO: 10	5'-CGAAGCTTGCTAGCCGAGTAGT	236-250
KY81	SEQ ID NO: 11	5'-CCGCAAGACTGCTAGCCGAGTAGT	227-250
KY88	SEQ ID NO: 12	5'-GTTGGGTCGCGAAAGGCCTTGTGGT	251-275
KY86	SEQ ID NO: 13	5'-GGTGCTTGCGAGTGCCCCGGGAGGTCTCGT	288-317
KY87	SEQ ID NO: 14	5'-GACTTCCGAGCGGTCGCAACCTCG	482-505

Table 2 lists oligonucleotides that function as negative sense (downstream) primers or as probes. The same internal ordering as in Table 1 is used.

Table 2

Oligo	Sequence Listing	Sequence	Position (nt)
KY153	SEQ ID NO: 15	5'-CCCAACACTACTCGGCTAGCAGTCT	232-256
KY149	SEQ ID NO: 16	5'-AAGGCCTTTCGCGACCCAACACTACT	245-278
KY148	SEQ ID NO: 17	5'-CACAAGGCCTTTCGCGACCCAACACT	248-273
KY78	SEQ ID NO: 18	5'-CTCGCAAGCACCCTATCAGGCAGT	276-299
KY145	SEQ ID NO: 19	5'-CACTCGCAAGCACCCTATCAGGCAGT	276-301
KY95	SEQ ID NO: 20	5'-GGGAATTCGCAAGCACCCTATCAGGCAGT	276-298
KY100	SEQ ID NO: 21	5'-CGAGGTTGCGACCGCTCGGAAGT	483-505
KY110	SEQ ID NO: 22	5'-AGGTTGCGACCGCTCGGAAGT	483-503
KY109	SEQ ID NO: 23	5'-AATGCCATAGAGGGGCCAAGG	573-593
KY111	SEQ ID NO: 24	5'-ATTGCCATAGAGGGGCCAAGG	573-594
KY99	SEQ ID NO: 25	5'-CAGAATTCATTGCCATAGAGGGGCCAAGGAT	570-592
KY68	SEQ ID NO: 26	5'-CAGAATTCGCCCTCATTGCCAT	586-599
KY82	SEQ ID NO: 27	5'-CCCACCCCAAGCCCTCATTGCCAT	586-610

Several of the oligonucleotides have hybridizing regions modified to include a restriction site toward the 5'-end of the molecule. The restriction site is introduced into the amplified product when one of these oligonucleotides is used as a primer. Initial hybridization conditions are chosen such that the base pair mismatches around the restriction site are tolerate Mismatches near the 5'-end are tolerated better than those near the 3'-end of a primer. The oligonucleotides KY65 (SEQ ID NO. 1), KY98 (SEQ ID NO. 3), KY96 (SEQ ID NO. 4), and KY67 (SEQ ID NO. 10) are upstream primers and contain a HindIII site. The oligonucleotides KY95 (SEQ ID NO. 20), KY99 (SEQ ID NO. 25), and KY68 (SEQ ID NO. 26) are downstream primers and contain an EcoRI site. The incorporation of such restriction sites into the amplified product facilitates cloning of the amplified product.

European Patent Application No. 92114115.6 provides a new HCV isolate. Most isolates are related to one of two strains of HCV. The first is a U.S. prototype strain described in European Publication Nos. 318,216, 388, 232, and 398, 748. The second is a Japanese strain described by Kato et al. supra. The two strains differ by up to 30% in regions of putative nonstructural genes, but show greater than 98% homology in the 5' untranslated region and 92% homology in the 5' portion of the capsid or core gene.

The isolate of European Patent Application No. 92114115.6 termed C9, is more distantly related to both strains. This new isolate is 93% similar to the consensus 5' untranslated region. It has only about 85% homology in the 5' portion of the core gene region with either the prototype or the Japanese strain (see Table 3, below).

The C9 (SEQ ID NO. 28) isolate and related isotypes, R45 (SEQ ID No. 30), R43 (SEQ ID NO. 32), R110 (SEQ ID NO. 31), and R116 (SEQ ID NO. 29) (see Figure 1), were cloned into the RI/HindIII restriction sites in pBS(+) purchased from Stratagene as described above. The variant viruses were cloned using purified viral DNA targets and PCR cloning methods as described in U.S. Patent No. 4,800,159. The resulting plasmids were transformed into E. coli strain DG101 (ATCC Deposit No. 47043).

Nucleotide sequences from the 5' untranslated sequence and the 5'-end of the capsid gene of the prototype C9 isolate and four related isolates are disclosed in C9 (SEQ ID NO. 28), R116 (SEQ ID NO. 29), R45 (SEQ ID No. 30), R110 (SEQ ID NO. 31), and R43 (SEQ ID. NO. 32) and shown below. The sequences shown do not include primers KY96 (SEQ ID NO. 4) and KY99 (SEQ ID NO. 25), which were used to facilitate cloning the viral sequences.

C9 - SEQ ID NO. 28

```
   1  ACTGTCTTCA CGCAGAAAGC GTCTAGCCAT GGCGTTAGTA TGAGTGTCGT
  51  ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA GCCATAGTGG TCTGCGGAAC
 101  CGGTGAGTAC ACCGGAATTA CCGGAAAGAC TGGGTCCTTT CTTGGATAAA
 151  CCCACTCTGT GTCCGGTCAT TTGGGCGTGC CCCCGCAAGA CTGCTAGCCG
 201  AGTAGCGTTG GGTTGCGAAA GGCCTTGTGG TACTGCCTGA TAGGGTGCTT
 251  GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GCATCATGAG CACAAATCCT
 301  AAACCTCAAA GAAAAACCAA AAGAAACACA AACCGCCGCC CACAGGACGT
 351  TAAGTTTCCG GGTGGCGGCC AGATCGTTGG CGGAGTTTAC TTGCTGCCGC
 401  GCAGGGGCCC CAGGTTGGGT GTGCGCGCGA CAAGAAAGAC TTCCGAGCGA
 451  TCCCAGCCGC GTGGGAGACG CCAGCCCATC CCAAAAGATC GGCGCTCCAC
 501  CGGCAAGTCC TGGGGAAAGC CAGGAT
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R116 - SEQ ID NO. 29

```
   1  GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA
  51  GCCATAGTGG TCTGCGGAAC CGGTGAGTAC GCCGAATTAC CGGAAAGACT
 101  GGGTCCTTTC TTGGATAAAC CCACTCTATG TCCGGTCATT TGGGCGTCCC
 151  CCGCAAGACT GCTAGCCGAG TAGCGTTGGG TTGCGAAAGG CCTTGTGGTA
 201  CTGCCTGATA GGGTGCTTGC GAGTGCCCCG GGAGGTCTCG TAGACCGTGC
 251  ATCATGAGCA CAGATCCTAA ACCTCAAAGA AAAACCAAAA GAAATACAAA
 301  CCGCCGCCCA CAGGACGTCA AGTTCCCGGG TGGCGGCCAG ATCGTTGGCG
 351  GAGTTTACTT GCTGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCACAACA
 401  AGGAAGACTT CCGAGCGATC CCAGCCGCGT GGAAGACGCC AGCCCATCCC
 451  GAAAGATCGG CGCTCCACCG GTAAGTCCTG GGGAAAGCCA GGAT
```

R45 - SEQ ID NO. 30

```
   1  GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA
  51  GCCATAGTGG TCTGCGGAAC CGGTGAGTAC GCCGAATTGC CGGAAAGACT
 101  GGGTCCTTTC TTGGATAAAC CCACTCTATG TCCGGTCATT TGGGCGTCCC
 151  CCGCAAGACT GCTAGCCGAG TAGCGTTGGG TTGCGAAAGG CCTTGTGGTA
 201  CTGCCTGATA GGGTGCTTGC GAGTGCCCAG GGAGGTCTCG TAGACCGTGC
 251  ATCATGAGCA CAAATCCTAA ACCCCAAAGA AAAACCAAAA GAAACACAAA
 301  CCGCCGCCCA CAGGACGTTA AGTTCCCGGG TGGCGGCCAG ATCGTTGGCG
 351  GAGTTTACTT GATGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCGCGACG
 401  AGGAAGACTT CCGAGCGATC CCAGCCGCGT GGGAGACGCC AGCCCATCCC
 451  GAAAGATCGG CGTTCCACCG GCAAGTCCTG GGGAAAGCCA GGAT
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R110 - SEQ ID NO. 31

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   1  GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA
  51  GCCATAGTGG TCTGCGGAAC CGGTGAGTAC GCCGAATTGC CGGAAAGACT
 101  GGGTCCTTTC TTGGATTAAC CCACTCTATG TCCGGTCATT TGGGCGTCCC
 151  CCGCAAGACT GCTAGCCTAG TAGCGTTGGG TTGCGAACGG CCTTGTGGTA
 201  CTGCCTGATA GGGTGCTTGC GAGTGCCCCG GGAGGTCTCG TAGACCGTGC
 251  ATCATGAGCA CAAATCCTAA ACCTCAAAGA AAAACCAAAA GAAACACAAA
 301  CCGCCGCCCA CAGGACGTCA AGTTCCCGGG AGGCGGTCAG ATCGTTGGCG
 351  GAGTTTACTT GCTGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCGCGACA
 401  AGGAAGACTT CCGAGCGATC CCAGCCGCGT GGGAGACGCC AGCCCATCCC
 451  GAAAGATCGG CGCTCCACCG GCAAGTCCTG GGGAAAGCCA GGAT
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R43 - SEQ ID NO. 32

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   1  GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA
  51  GCCATAGTGG TCTGCGGAAC CGGTGAGTAC ACCGAATTAC CGGAAAGACT
 101  GGGTCCTTTC TTGGATAAAC CCACTCTATG TCCGGTCATT TGGGCGTCCC
 151  CCGCAAGACT GCTAGCCTAG TAGCGTTGGG TTGCGAACGG CCTTGTGGTA
 201  CTGCCTGATA GGGTGCTTGC GAGTGCCCCG GGAGGTCTCG TAGACCGTGC
 251  ATCATGAGCA CAAATCCTAA ACCTCAAAGA AAAACCAAAA GAAACACAAA
 301  CCGCCGCCCA CAGGACGTCA AGTTCCCGGG TGGCGGCCAG ATCGTTGGCG
 351  GAGTTTACTT GCTGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCGCGACA
 401  AGGAAGACTT CCGAACGGTC CCAGCCGCGT GGGAGGCGCC AGCCCATCCC
 451  AAAAGATCGG CGCTCCACCG GCAAGTCCTG GGGAAAGCCA GGAT
```

Clones containing the viral sequences have been deposited with the American Type Culture Collection, Baltimore, Maryland as follows:

Isolate	SEQ ID NO.	Plasmid Designation	ATCC Deposit No.	Date of Deposit
C9	28	pHCV-C9	75265	July 2, 1992
R110	31	pHCV-R110	75266	July 2 , 1992

Plasmid pHCV-C9 contains the novel variant C9 sequence. The alignment of the four related variants with the C9 sequences is shown in Figure 1. The source of the sequence data for known isolates was as follows: HCV-J1, HCV-J4 (Okamoto et al., 1990, Japan J. Exp. Med. 6(3):167-177); HCV-J (Kato et al., 1990, Mol. Biol. Med. 7:495-501); HCV-BK (Takamizawa et al., 1991, J. Virol. 65:1105-1113); and HCV-1 US-PT (Han et al., 1991, Proc. Natl. Acad. Sci. USA 88:1711-1715)

The numbering is according to Kato et al., 1990, Proc. Natl. Acad. Sci. USA 87:9524-9528.

Table 3

Determination of nucleotide and amino acid sequence homology of C9 isolate to prototype US (PT-HCV) and Japanese isolates (J-HCV).			
Sequences	**Isolate**	**PT-HCV**	**J-HCV**
5' UTR			
nucleotide (255)	C9	92.9%	92.9%
	J-HCV	98.8%	---
Core			
nucleotide (244)	C9	84.9%	85.1%
	J-HCV	92.1%	---
amino acid (80)	C9	91.3%	90.0%
	J-HCV	98.7%	---

European Patent Application No. 92114115.6 provides materials and methods for assays that are specific to the C9 isolate and distinguish the isolate from other hepatitis isolates. Said methods are based on nucleic acid hybridization with or without the use of PCR to amplify the targeted sequences. In other embodiments, the methods use immunoglobulins specific to the C9 isolate.

The oligonucleotide sequences of primers and probes specific to C9 are presented in Table 4, below.

Table 4

Probes		
SEQ ID NO. 36	MY160 5'- TGTCCGGTCATTTGGGCG - 3'	(nt216-233)
SEQ ID NO. 33	(1) 5'-TTGCCGGAAAGACTGGGTCCTTTC-3'	(nt174-197)
SEQ ID NO. 34	(2) 5'-CAAAAGAAACACAAACCGCCGCCC-3'	(nt374-397)
SEQ ID NO. 35	(3) 5'-CCAGCCCATCCCGAAAGATCGGCG-3'	(nt527-550)
Upstream Primers		
SEQ ID NO. 37	(1) 5'-AAACCCACTCTATGTCCGGTC-3'	(nt204-224)
SEQ ID NO. 38	(2) 5'-GTACGCCGGAATTGCCGGAAA-3'	(nt163-183)
SEQ ID NO. 39	(3) 5'-CCTCAAAGAAAAACCAAAAGA-3'	(nt360-380)
Downstream Primers		
SEQ ID NO. 40	(4) 5'-TGGCGTCTCCCACGCGGCTGG-3'	(nt509-529)
SEQ ID NO. 41	(5) 5'-CTTTCCCCAGGACCTGCCGGT-3'	(nt555-575)

The numbering system used to identify the nucleotides is from Kato et al., 1990, Proc. Natl. Acad. Sci., supra.

One oligonucleotide, KY150 (SEQ ID NO. 42), is useful for the detection of both the C9 isolate and the previously known HCV prototype isolates. This oligonucleotide has the following sequence:
5'- CATAGTGGTCTGCGGAACCGGTGAGT - 3'.

It will be apparent to one of skill in the art that any upstream/downstream primer pair shown in Table 4 is suitable for specifically amplifying the C9 isolate and related isotypes. It will be additionally apparent to select a C9-specific probe suitable for hybridizing the amplified nucleic acid subsequence using as guidance the nucleotide positions provided in Table 4.

In a preferred embodiment, the primers of the invention are used in conjunction with a polymerase chain reaction

(PCR) amplification of the target nucleic acid. Because HCV is an RNA virus, the first step in the amplification is the synthesis of a DNA copy (cDNA) of the region to be amplified. Reverse transcription can be carried out as a separate step, or, as described below, in a homogeneous reverse transcription-polymerase chain reaction (RT-PCR), a modification of the polymerase chain reaction for amplifying RNA.

Although the PCR process is well known in the art (see U.S. Patent Nos. 4,683,195; 4,683,202; and 4,965,188, some general PCR information is provided below for purposes of clarity and full understanding of the invention for those unfamiliar with the PCR process.

To amplify a target nucleic acid sequence in a sample by PCR, the sequence must be accessible to the components of the amplification system. In general, this accessibility is ensured by isolating the nucleic acids from the sample. A variety of techniques for extracting ribonucleic acids from biological samples are known in the art. For example, see those described in Rotbart et al., 1989, in PCR Technology (Erlich ed., Stockton Press, New York) and Han et al. 1987, Biochemistry 26:1617-1625. Alternatively, if the sample is fairly readily disruptable, the nucleic acid need not be purified prior to amplification by the PCR technique, i.e., if the sample is comprised of cells, particularly peripheral blood lymphocytes or monocytes, lysis and dispersion of the intracellular components may be accomplished merely by suspending the cells in hypotonic buffer.

The first step of each cycle of the PCR involves the separation of the nucleic acid duplex. Of course, if the target nucleic acid is single- stranded, i.e., single-stranded RNA, no initial separation step is required during the first cycle. Once the strands are separated, the next step in PCR involves hybridizing the separated strands with primers that flank the target sequence. The primers are then extended to form complementary copies of the target strands. For successful PCR amplification, the primers are designed so that the position at which each primer hybridizes along a duplex sequence is such that an extension product synthesized from one primer, when separated from the template (complement), serves as a template for the extension of the other primer. The cycle of denaturation, hybridization, and extension is repeated as many times as necessary to obtain the desired amount of amplified nucleic acid.

In the preferred embodiment of the PCR process, strand separation is achieved by heating the reaction to a sufficiently high temperature for an sufficient time to cause the denaturation of the duplex but not to cause an irreversible denaturation of the polymerase (see U.S. Patent No. 4,965,188). Typical heat denaturation involves temperatures ranging from about 80°C to 105°C for times ranging from seconds to minutes. Strand separation, however, can be accomplished by any suitable denaturing method including physical, chemical, or enzymatic means. Strand separation may be induced by a helicase, for example, or an enzyme capable of exhibiting helicase activity. For example, the enzyme RecA has helicase activity in the presence of ATP. The reaction conditions suitable for strand separation by helicases are known in the art (see Kuhn Hoffman-Berling, 1978, CSH-Quantitative Biology 43:63-67; and Radding, 1982, Ann. Rev. Genetics 16:405-436).

Template-dependent extension of primers in PCR is catalyzed by a polymerizing agent in the presence of adequate amounts of four deoxyribonucleoside triphosphates (typically dATP, dGTP, dCTP, and dTTP) in a reaction medium comprised of the appropriate salts, metal cations, and pH buffering system. Suitable polymerizing agents are enzymes known to catalyze template-dependent DNA synthesis. Because Hepatitis C is an RNA virus, the initial template for primer extension is RNA. Polymerizing agents suitable for synthesizing a complementary, copy-DNA (cDNA) sequence from the RNA template are reverse transcriptase (RT), such as avian myeloblastosis virus RT, Moloney murine leukemia virus RT, or Thermus thermophilus (Tth) DNA polymerase, a thermostable DNA polymerase with reverse transcriptase activity marketed by Perkin Elmer. Typically, the genomic RNA/cDNA duplex template is heat denatured during the first denaturation step after the initial reverse transcription step leaving the DNA strand available as an amplification template. Suitable polymerases for use with a DNA template include, for example, E. coli DNA polymerase I or its Klenow fragment, T_4 DNA polymerase, Tth polymerase, and Taq polymerase, a heat-stable DNA polymerase isolated from Thermus aquaticus and developed and manufactured by Hoffmann-La Roche and commercially available from Perkin Elmer. The latter enzyme is widely used in the amplification and sequencing of nucleic acids. The reaction conditions for using Taq polymerase are known in the art and are described in Gelfand, 1989, PCR Technology, supra.

When RNA is amplified, an initial reverse transcription (RT) step is carried out to create a DNA copy (cDNA) of the RNA. PCT patent publication No. WO 91/09944, published July 11, 1991 describes high-temperature reverse transcription by a thermostable polymerase that also functions in PCR amplification. High-temperature RT provides greater primer specificity and improved efficiency. In a "homogeneous RT-PCR" the same primers and polymerase suffice for both the reverse transcription and the PCR amplification steps, and the reaction conditions are optimized so that both reactions occur without a change of reagents. Thermus thermophilus DNA polymerase, a thermostable DNA polymerase that can function as a reverse transcriptase, is used for all primer extension steps, regardless of template. Both processes can be done without having to open the tube to change or add reagents; only the temperature profile is adjusted between the first cycle (RNA template) and the rest of the amplification cycles (DNA template).

The 5' terminal end of the HCV genome is predicted to have significant secondary structure that could hinder reverse transcription with a reverse transcriptase such as Moloney murine leukemia virus RT by interfering with primer hybridization. Unfortunately, raising the reaction temperature to denature the secondary structure also inactivates most reverse transcriptase enzymes. The use of the reverse transcriptase activity of recombinant Thermus thermophilus

(rTth) DNA polymerase allows the cDNA synthesis to take place at elevated temperatures without enzyme inactivation. The primers of the present invention remain hybridized to the RNA template at this elevated reverse transcription temperature.

The PCR method can be performed in a step-wise fashion, where after each step new reagents are added, or in a fashion where all of the reagents are added simultaneously, or in a partial step-wise fashion, where fresh or different reagents are added after a given number of steps. For example, if strand separation is induced by heat, and the polymerase is heat-sensitive, then the polymerase has to be added after every round of strand separation. However, if, for example, a helicase is used for denaturation, or if a thermostable polymerase is used for extension, then all of the reagents may be added initially, or, alternatively, if molar ratios of reagents are of consequence to the reaction, the reagents may be replenished periodically as they are depleted by the synthetic reaction.

Those skilled in the art will know that the PCR process is most usually carried out as an automated process with a thermostable enzyme. In this process, the temperature of the reaction mixture is cycled through a denaturing region, a primer annealing region, and an extension reaction region. Alternatively, the annealing and extension temperature can be the same. The RT-PCR described in the examples uses such a two-step temperature cycling. A machine specifically adapted for use with a thermostable enzyme is commercially available.

Those skilled in the art will also be aware of the problems of contamination of a PCR by the amplified nucleic acid from previous reactions and nonspecific amplification. A method to reduce these problems allows the enzymatic degradation of any amplified DNA from previous reactions and reduces nonspecific amplification. The PCR amplification is carried out in the presence of dUTP instead of dTTP. The resulting double-stranded, uracil-containing product is subject to degradation by uracil N-glycosylase (UNG), whereas normal thymine-containing DNA is not degraded by UNG. Adding UNG to the amplification reaction mixture before the amplification is started degrades all uracil-containing DNA that might serve as target. Because the only source of uracil-containing DNA is the amplified product of a previous reaction, this method effectively sterilizes the reaction mixture, eliminating the problem of contamination from previous reactions (carryover). UNG itself is rendered temporarily inactive by heat, so the denaturation steps in the amplification procedure also serve to inactivate the UNG. New amplification products, therefore, though incorporating uracil, are formed in an effectively UNG-free environment and are not degraded.

A preferred embodiment of the invention utilizes a homogeneous RT/PCR method which incorporates a sterilization step. This one tube, non-addition reaction serves to sterilize the RT-PCR reaction preventing carryover contamination and providing amplified detectable PCR product from a sample containing an RNA target. This method is exemplified in Example 6.

Although the preferred embodiment incorporates RT-PCR amplification, amplification of target sequences in a sample may be accomplished by any known method, such as ligase chain reaction (LCR), transcription amplification, and self-sustained sequence replication, each of which provides sufficient amplification so that the target sequence can be detected by nucleic acid hybridization to an SSO probe. Alternatively, methods that amplify the probe to detectable levels can be used, such as Qβ-replicase amplification. The term "probe" encompasses the sequence specific oligonucleotides used in the above procedures; for instance, the two or more oligonucleotides used in LCR are "probes" for purposes of the present invention, even though some embodiments of LCR only require ligation of the probes to indicate the presence of an allele.

Sequence-specific probe hybridization is an important step in the successful performance of the present methods. The sequence specific oligonucleotide probes of the present invention hybridize specifically with a particular segment of the HCV genome and have destabilizing mismatches with the sequences from other organisms. Under sufficiently stringent hybridization conditions, the probes hybridize specifically only to exactly complementary sequences. The stringency of the hybridization conditions can be relaxed to tolerate varying amounts of sequence mismatch. Detection of the amplified product utilizes this sequence-specific hybridization to insure detection of only the correct amplified target, thereby decreasing the chance of a false positive caused by the presence of homologous sequences from related organisms.

The assay methods for detecting hybrids formed between SSO probes and nucleic acid sequences can require that the probes contain additional features in addition to the hybridizing region. For example, if the probe is first immobilized, as in the "reverse" dot blot format described below, the probe can also contain long stretches of poly-dT that can be fixed to a nylon support by irradiation, a technique described in more detail in PCT Patent Publication No. 89/11548. In the dot blot format, immobilized target is hybridized with probes containing a compound used in the detection process, as discussed below.

The probes of the invention can be synthesized and labeled using the techniques described above for synthesizing oligonucleotides. The probe can be labeled at the 5'-end with ^{32}P by incubating the probe with ^{32}P-ATP and kinase. A suitable nonradioactive label for SSO probes is horseradish peroxidase (HRP). Methods for preparing and detecting probes containing this label are described in the Examples below and in U.S. Patent Nos. 4,914,210 and 4,962,029. For additional information on the use of such labeled probes, see U.S. Patent No. 4,789,630; Saiki et al, 1988, N. Eng. J. Med. 319:537-541; and Bugawan et al., 1988, Bio/Technology 6:943-947. Useful chromogens include red leuco dye and 3,3',5,5'-tetramethylbenzidine (TMB).

The probes of the invention can be used to determine if viral sequences are present in a sample by determining if the SSO probes bind to the viral sequences present in the sample. Suitable assay methods for purposes of the present invention to detect hybrids formed between SSO probes and nucleic acid sequences in a sample are known in the art. For example, the detection can be accomplished using a dot blot format, as described in the Examples. In the dot blot format, the unlabeled amplified sample is bound to a solid support, such as a membrane, the membrane incubated with labeled probe under suitable hybridization conditions, the unhybridized probe removed by washing, and the filter monitored for the presence of bound probe. When multiple samples are analyzed with a single probe, the dot blot format is quite useful. Many samples can be immobilized at discrete locations on a single membrane and hybridized simultaneously by immersing the membrane in a solution of probe.

An alternate method that is quite useful when large numbers of different probes are to be used is a "reverse" dot blot format, in which the amplified sequence contains a label, and the probe is bound to the solid support. This format would be useful if the test of the present invention were used as one of a battery of tests to be performed simultaneously. In this format, the unlabeled SSO probes are bound to the membrane and exposed to the labeled sample under appropriately stringent hybridization conditions. Unhybridized labeled sample is then removed by washing under suitably stringent conditions, and the filter is then monitored for the presence of bound sequences.

Both the forward and reverse dot blot assays can be carried out conveniently in a microtiter plate. The probes can be attached to bovine serum albumin (BSA), for example, which adheres to the microtiter plate, thereby immobilizing the probe.

In another suitable assay system a labeled probe is added during the PCR amplification process. Any SSO probe that hybridizes to target DNA during each synthesis step is degraded by the 5' to 3' exonuclease activity of a polymerase, e.g., Taq polymerase. The degradation product from the probe is then detects. Thus, the presence of the breakdown product indicates that the hybridization between the SSO probe and the target DNA occurred.

The nucleotide sequences provided above are an important aspect of the present invention. Although only one strand of the sequence is shown, those of skill in the art recognize that the other strand of the sequence can be inferred from the information depicted above. This information enables the construction of other probes and primers of the invention.

The present invention also relates to kits, multicontainer units comprising useful components for practicing the present method. A useful kit can contain SSO probes for detecting Hepatitis C virus nucleic acid. In some cases, the SSO probes may be fixed to an appropriate support membrane. The kit can also contain primers for RT-PCR, as such primers are useful in the preferred embodiment of the invention. Other optional components of the kit include, for example, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. In addition to the above components, the kit can also contain instructions for carrying out the present method.

Example 1

In the homogeneous RT-PCR, the same polymerase functions as both a reverse transcriptase and a DNA polymerase. This allows both the initial reverse transcription of the HCV genomic RNA and the subsequent amplification of the cDNA to be performed in the same tube without opening the tube in between steps to change reagents.

Nucleic acids were isolated from serum or plasma using the IsoQuick™ nucleic acid extraction kit from MicroProbe. All amplifications were done using a TC9600 Thermocycler™ and MicroAmp™ tubes, both from Perkin Elmer, in total reaction volumes of 20 µl. The reagents for each 20 µl reaction are listed in Table 5, below.

Table 5

RT-PCR Reaction Mixture:	
H_20	6.3 µl
10x RT Reaction Buffer (100 mM Tris-HCl (pH 8.3), 900 mM KCl)	2.0 µl
$MnCl_2$ (10 mM, 0.85 mM final concentration)	1.7 µl
dNTP (2 mM each of dATP, dCTP, dGTP, and dTTP in H_20, pH 7.0)	2.0 µl
Primer KY78 (SEQ ID NO. 18) (1.5 µM in H_20, 3 picomole/reaction final concentration)	2.0 µl
Primer KY80 (SEQ ID NO. 5) (1.5 µM in H_20, 3 picomole/reaction final concentration)	2.0 µl
rTth DNA polymerase (Perkin Elmer, Norwalk, CT, USA; 0.18 µM or 2.5 units/µl in 1X Enzyme storage buffer (20 µM Tris-HCl (pH 7.5), 100 mM KCl, 0.1 µM EDTA, 1 µM DTT, 0.2% Tween™ 20 (Pierce Surfactants), 50% glycerol [v/v])	2.0µl
Template nucleic acid (<250 ng total in dH_2O)	2.0 µl

The TC9600 was programmed to provide the following reaction temperature profile. After preheating to 70°C for 1 minute, the program was paused long enough to insert the reaction tubes, the program was restarted, and the reaction was held at 70°C for 15 minutes to allow for reverse transcription. The reaction temperature was then raised to 95°C for 1 minute to denature the RNA-cDNA duplex. Next, the reaction temperature underwent two cycles of 95°C for 15 seconds and 60°C for 20 seconds followed by 38 cycles of 90°C for 15 seconds and 60°C for 20 seconds. Finally, the reaction temperature was held at 60°C for 4 minutes for the final extension step, cooled to 15°C, and held at that temperature until the analysis of the amplified sample could be performed.

Example 2

Using the dot blot format detection method, a small portion of the amplified DNA is denatured and applied to a nylon filter, which is then hybridized to a labeled probe. The probe hybridizing region is KY88 (SEQ ID NO. 12), and the probe is radioactivity labeled with ^{32}P. Alternatively, the probe can be covalently conjugated to horseradish peroxidase (HRP)to provide a means of nonisotopic detection in the presence of a chromogenic or chemiluminescent substrate.

The amplification reaction is generally carried out as described in Example 1. The PCR-amplified product is then denatured by treatment with alkali. To 5 µl of PCR product is added 5 µl of 0.5 M EDTA, pH 8.0, 8 µl of 5 N NaOH, and 82 µl H_20. The mixture is allowed to stand at room temperature for 10 minutes to complete the denaturation.

BioDyne™ B nylon filters (Pall Corp., Glen Cove, NY, USA) are prepared by soaking in H_2O for 5 to 10 minutes and further rinsing with 200 µl of H_2O after the dotblot manifold (Bio-Dot™ from Bio Rad, Richmond, CA, USA) has been set up. After denaturation, 100 µl of the sample mixture is applied under vacuum to the nylon membrane using the dot blot apparatus. Each well is then rinsed with 200 µl of 0.4 N NaOH and the entire filter is rinsed briefly with 2X SSC, and air-dried until no pools of liquid are left. The DNA is immobilized and cross-linked to the nylon filter by ultraviolet irradiation at a flux of 1200 mJ/cm^2 with a Stratalinker™ (Stratagene, La Jolla, CA, USA) UV light box (the "autocrosslink" setting).

Filters are "pre-hybridized" by soaking in the hybridization buffer (5X SSPE, 5X Denhardt's solution, 0.1% SDS, 50 µg/ml herring sperm DNA) in heat-sealable bags at 50°C (air shaker) for at least 30 minutes. The buffer is then replaced with an equal amount of the same solution containing 1-2 x 10^5 cpm/ml probe, and the filter is allowed to hybridize between 2 hours and overnight at 50°C.

After hybridization, filters are washed three times in 2X SSPE/0.1% SDS; twice for 20 minutes at room temperature, and then once for twenty minutes at the high stringency temperature of 60°C. The filters are then blotted dry, wrapped in plastic wrap, and exposed to X-ray film at -70°C with one or two intensifying screens.

An alternate method of visualization is to hybridize with horseradish peroxidase conjugated oligonucleotide probes, prepared as described by Levenson and Chang, 1989, in PCR Protocols: A Guide to Methods and Applications (Innis et al., eds., Academic Press, San Diego), pages 92-112, and Saiki et al., 1988, N. Eng. J. Med. 319:537-541, each of which is incorporated herein by reference. Hybridization is carried out with 2 pmoles of HRP-SSO probe per 5 ml of hybridization solution.

After washing, filters to be developed with a chromogenic dye substrate are rinsed in 100 mM sodium citrate, pH 5.0, then placed in 100 mM sodium citrate, pH 5.0, containing 0.1 mg/ml of 3,3',5,5'-tetramethylbenzidine per milliliter (Fluka) and 0.0015 percent hydrogen peroxide, and incubated with gentle agitation for 10 to 30 minutes at room tem-

perature. Developed filters are rinsed in water and immediately photographed. The TMB detection system is prepared and used substantially as described in the AmpliType™ DQα DNA typing kit marketed by Perkin Elmer. In another embodiment, filters are developed with the chemiluminescent detection system (ECL; Amersham, Arlington Heights, IL, USA). Filters are rinsed in PBS for 5 minutes and placed in the ECL solution for 1 minute with gentle agitation. Filters are then exposed to X-ray film at room temperature for 1 to 5 minutes.

Example 3

In this embodiment of the invention, the reverse dot blot format is being used. The probe hybridization region is KY88 (SEQ ID NO. 12), KY150 (SEQ ID NO. 42), or MY160 (SEQ ID NO.36), and the probe is fixed to a membrane. The amplified target DNA is hybridized to the membrane-bound probe as described in Saiki et al., 1989, Proc. Natl. Acad. Sci. 86:6230-6234; and in the product insert of the AmpliType® DQalpha DNA typing kit marketed by Perkin Elmer. The amplification primers are biotinylated, as described in Levenson and Chang, 1989, supra, so that any amplified DNA that hybridizes to the membrane-bound probes can be easily detected.

In one embodiment, detection is carried out by reacting streptavidin conjugated horseradish peroxidase (SA-HRP) with any biotinylated, amplified DNA hybridized to the membrane-bound probe. The HRP thus becomes bound, through the SA-biotin interaction, to the amplified DNA and can be used to generate a signal by a variety of well-known means, such as the generation of a colored compound by the oxidation of tetramethylbenzidine (see U.S. Patent No. 4,789,630).

Although the probe can be fixed to the membrane by any means, a preferred method involves "tailing" the probe hybridizing region with a much longer sequence of poly-dT. The resulting poly-dT "tail" can then be reacted with amine groups on a nylon membrane to fix the probe covalently to the membrane. This reaction can be facilitated by UV irradiation.

Terminal deoxyribonucleotidyl transferase (TdT, Ratliff Biochemicals; for the reactions below assume a concentration of about 120 Units/μl, which is 100 pmole/μl) can be used to create a poly-dT tail on a probe, although one can also synthesize the tailed probe on a commercially available DNA synthesizer. When one uses a DNA synthesizer to make the tailed probe, however, one should place the tail on the 5'-end of the probe, so that undesired premature chain termination occurs primarily in the tail region.

TdT reactions should be carried out in a volume of about 100 μl containing 1X TdT salts, 200 pmole of oligonucleotide, 800 μM DTT, and 60 units of TdT. 10X TdT salts is 1,000 mM K-cacodylate, 10 mM $CoCl_2$, 2 mM dithiothreitol, 250 mM Tris-Cl, pH 7.6, and is prepared as described by Roychoudhury and Wu, Meth. Enzymol. 65: 43-62. A 10X stock solution of 8 mM dTTP can be prepared (neutralized to pH 7 with NaOH) for convenience.

The TdT reaction should be carried out at 37°C for two hours and then stopped by the addition of 100 μl of 10 mM EDTA, pH 8. The final concentration of tailed oligonucleotide is 1 μM (1 pmole/μl), and the length of the homopolymer tail is about 400 residues. Tail length can be changed by adjusting the molar ratio of dTTP to oligonucleotide. The tailed probes can be stored at -20°C until use.

The nylon membrane preferred for the reverse dot blot format is the Biodyne™ B nylon membrane, 0.45 micron pore size, manufactured by Pall and also marketed by ICN as the BioTrans™ nylon membrane. The probes can be spotted onto the membrane very conveniently with the Bio-Dot™ dot blot apparatus manufactured by BioRad. Each probe is spotted onto a unique, discrete location on the membrane. About 2 to 10 picomoles of each tailed probe is premixed with 50 to 100 μl of TE buffer before application to the dot blot apparatus. After dot blotting, the membrane is briefly placed on absorbent paper to draw off excess liquid. The membrane is then placed inside a UV light box, such as the Stratalinker™ light box manufactured by Stratagene, and exposed to 50 to 60 millijoules/cm^2 of flux at 254 nm to fix the tailed probe to the nylon membrane. After a brief rinse for about 15 minutes in hybridization solution to remove unbound probe, the membrane is then ready for hybridization with biotinylated PCR product.

Amplified PCR products are denatured by heating to 95°C for 3 to 10 minutes and 40 μl of the denatured PCR product are added to each probe panel for hybridization. Hybridization is carried out at 57°C for 20 minutes in a shaking water bath in a hybridization buffer composed of 0.5X SSPE, 0.25% SDS, and 5X Denhardt's solution (20X SSPE contains 0.02 M EDTA, 0.2 M NaH_2PO_4, 3.6 M NaCl, 0.11 M NaOH, adjusted to pH 7.4). The hybridization buffer is replaced with 3 ml of a solution consisting of 25 μl of SA-HRP in 3.1 ml hybridization buffer, and incubated for 20 minutes at 57°C in a shaking water bath.

Washing is carried out in a wash buffer of 2X SSPE and 0.1% SDS. After a brief rinse of the membrane in 10 ml of wash buffer, a 12 minute stringent wash in 10 ml of buffer is done at 57°C. Another 5 minute room temperature wash is then carried out, followed by a 5 minute wash in 10 ml of 0.1 M sodium citrate, pH 5.0.

Chromogen binding is carried out in 5 ml of chromogen solution consisting of 5 ml of 0.1 M sodium citrate, 5 μl of 3% hydrogen peroxide, and 0.25 ml chromogen (TMB from Perkin Elmer) for 25-30 minutes at room temperature. Three 10 minute washes in distilled water are carried out at room temperature. A post-wash of 1X PBS at room temperature for 30 minutes can enhance signal quality. During these steps involving the chromogen, the membrane should be shielded from light by a aluminum foil covering. The developed membrane should be photographed for a permanent

record.

Example 4

In this embodiment of the invention a microtiter plate format is being used. The probe is fixed to a well of a microtiter plate. The amplified target DNA is hybridized to the bound probe as described above. As in the previous example, the amplification primers are biotinylated, to allow detection of amplified DNA that hybridizes to the bound probes.

The desired probes conjugated to BSA are first allowed to absorb to the plastic surface of the individual wells. The wells are then blocked with protein, such as bovine serum albumin. Preferably, 96 well plates available from Corning are used.

Once the amplification has been completed, the PCR tubes were removed from the thermocycler (available through Perkin Elmer). One hundred microliters of denaturation solution were added to each PCR tube. A new pipette tip is used for each tube. In one embodiment, detection may not be preformed immediately. In that case, the PCR tubes were stored overnight at 2°C to 8°C. Denatured amplification reactions become viscus upon storage at 2°C to 8°C. Tubes were briefly warmed at 25°C to 30°C prior to opening tubes to make pipette easy.

The appropriate number of eight well microtiter plate strips (minimally 2 strips) were removed and set into the microtiter plate frame. One hundred microliters of hybridization buffer was pipetted into each well of the microtiter plate.

The denaturation solution contains 0.4 M NaOH; 80 mM EDTA and 0.005% Thymol blue. Hybridization/neutralization buffer contains: 2.5 M NaSCN; 80 mM NaH_2PO_4; 10 mM NaH_2PO_4; and 0.125% Tween™ 20. Before use the pH is checked to be 5.0 +/- 0.2.

Using plugged tips with a multi channel pipetter, 25 µl of the denatured amplification reaction from each PCR tube in the tray was pipetted to the corresponding well position in the microtiter plate. The plate was covered with the microtiter plate lid and gently tapped on the side 10 to 15 times. Wells in which proper reagent pipetting has been done will turn light yellow in color. If no or only a single change in blue color is noted, excess amplicon has been added. The test is continued as positive OD values will increase but negative OD values are not affected. The plate was incubated for 60 minutes at 37°C.

Following incubation the plate was washed five times with wash solution. Washing of the plate may be preformed manually or with an automated microtiter plate washer programmed accordingly. For washing, a 1X PCR wash buffer was used. A 10X concentrate of PCR washed buffer was prepared as follows: 9.94 grams per liter of sodium phosphate dibasic; 4.41 grams per liter sodium phosphate (monobasic); 3.722 grams per liter EDTA; 87.66 grams per liter sodium chloride; 13.7 grams per liter of Tween™ 20; and 10 grams per liter of Pro Clin 300 (Rohm and Haas, Philadelphia, PA). The solution is pH adjusted with phosphoric acid (pH 6.5 - 7.1 is preferred).

For manual washing the contents of the plate were emptied and tapped dry. Three hundred microliters of wash solution was added to each well in the plate being tested, and the plate was allowed to dry for 15 to 30 seconds. The plate was again emptied and tapped dry. This wash process was repeated four additional times.

For an automated microplate washer, the following procedure was used. The contents of the wells was aspirated. The washer was programmed to add 350 microliters of working wash solution to each well in the plate being tested and soaked for 30 seconds and aspirated. The steps were repeated four additional times. The plate was then tapped dry.

One hundred microliters of conjugate was added to each well in the plate being tested. The avidin-HRP conjugate is prepared as follows. The diluent contains 0.1 molar; 0.25% Emulsit 25 (DKS International, Inc., Tokyo, Japan); 1.0% Kathon CG (Rohm and Haas, Philadelphia, PA); 0.1% phenol; 1.0% bovine gamma globulin. The solution was pH adjusted to 7.3 with concentrated HCl. To this diluent 10 nM of conjugated avidin was added (Vector Labs, Burlingame, CA). The plate was then covered and then incubated 50 minutes at 37°C and again washed as described above. The working substrate was prepared by mixing 2.0 ml of Substrate A and 0.5 ml of Substrate B for each multiple of two 8 well microtiter plate strips (16 tests). Substrate A contains 3 mM hydrogen peroxide; 6.5 mM citrate and 0.1% Kathon CG. Substrate B contains 4.2 mM 3,3',5,5' tetramethylbenzidine and 40% dimethylformamide. The working substrate was prepared no more than three hours before use and was stored away from direct sunlight.

One hundred microliters of working substrate (substrate A and B mixture) was added to each well of the plate being tested. The plate was then covered and incubated in the dark for 10 minutes at room temperature (20°C to 25°C). One hundred microliters of Stop Reagent (5% H_2SO_4) was added to each well being tested. The absorbance of each well of 450 mM was read within one hour of adding the Stop Reagent. The absorbance value was recorded for specimen and control.

Example 5

The oligonucleotides of the present invention provide numerous combinations of primers and probes that can be used in the amplification of HCV genomic sequences and detection of the amplified product. A large number of oligonucleotides have been tested for effectiveness as primers in an RT-PCR amplification.

PCR amplification reactions were carried out with various pairs of oligonucleotides using the methods described in

Example 1. Amplified product was detected by standard methods of agarose gel electrophoresis separation and staining (see Sambrook et al., supra). Each of the upstream primers KY65 (SEQ ID NO. 1) and KY98 (SEQ ID NO. 3) functioned effectively with each of the downstream primers KY68 (SEQ ID NO. 26), KY95 (SEQ ID NO.20), and KY99 (SEQ ID NO. 25) in the amplification of HCV sequences. KY67 (SEQ ID NO. 10) functioned effectively with both KY68 (SEQ ID NO. 26) and KY99 (SEQ ID NO. 25). Each of the upstream primers KY80 (SEQ ID NO. 5), KY83 (SEQ ID NO. 7), KY84 (SEQ ID NO. 8), KY85 (SEQ ID NO. 9), and KY144 (SEQ ID NO. 6) functioned effectively with each of the downstream primers KY78 (SEQ ID NO. 18), KY95 (SEQ ID NO. 20), KY145 (SEQ ID NO. 19), KY148 (SEQ ID NO. 17), and KY149 (SEQ ID NO. 16). Finally, each of the upstream primers KY80 (SEQ ID NO. 5) and KY81 (SEQ ID NO. 11) functioned effectively with KY100 (SEQ ID NO. 21).

Amplification product from PCR amplification using KY78 (SEQ ID NO. 18) and KY80 (SEQ ID NO. 5) as primers was detected by probing with each of KY88 (SEQ ID NO. 12), KY84 (SEQ ID NO. 8), and KY85 (SEQ ID NO. 9) using the methods described in Example 2, above.

Primers KY153 (SEQ ID NO. 15), KY149 (SEQ ID NO. 16), and KY148 (SEQ ID NO. 17) cannot be used with any of the upstream primers that are downstream of KY85. The 3'-end of KY78 (SEQ ID NO. 18) is adjacent to the 3'-end of KY88 (SEQ ID NO. 12), so although these two primers could function as a primer pair, the lack of any intervening sequence makes independent probing impossible. Primer KY86 (SEQ ID NO. 13) can only be paired with KY100 (SEQ ID NO. 21), KY99 (SEQ ID NO. 25), KY109 (SEQ ID NO. 23), and KY111 (SEQ ID NO. 24). Primer KY87 (SEQ ID NO. 14) can only be paired with KY99 (SEQ ID NO. 25), KY109 (SEQ ID NO. 23), and KY111 (SEQ ID NO. 24).

KY84 (SEQ ID NO. 8), KY85 (SEQ ID NO. 9), KY87 (SEQ ID NO. 14), and KY148 (SEQ ID NO. 17) discussed above are useful for the detection of known HCV isolates other than the C9 isolate. The probes and primers disclosed in Table 4 are specific for amplifying and detecting HCV-C9 and related variants and for excluding Japan and U.S. HCV prototypes.

Primers for specifically amplifying Japan and U.S. HCV prototypes and not HCV-C9 are exemplified by KY84 (SEQ ID NO. 8), KY85 (SEQ ID NO. 9), KY148 (SEQ ID NO. 17) and KY87 (SEQ ID NO. 14). Primers for amplifying Japan, U.S., and C9 HCV prototypes include KY67 (SEQ ID NO. 10), KY78 (SEQ ID NO. 18), KY80 (SEQ ID NO. 5), KY81 (SEQ ID NO. 11), KY83 (SEQ ID NO. 7), KY86 (SEQ ID NO. 13), KY88 (SEQ ID NO. 12), KY95 (SEQ ID NO. 20), KY100 (SEQ ID NO. 21), KY144 (SEQ ID NO. 6), KY145 (SEQ ID NO. 19), and KY153 (SEQ ID NO. 15). Primers KY65 (SEQ ID NO. 1), KY68 (SEQ ID NO. 27), KY98 (SEQ ID NO. 3), KY99 (SEQ ID NO. 25), KY109 (SEQ ID NO. 23), KY111 (SEQ ID NO. 24), and KY149 (SEQ ID NO. 16) are suitable for amplifying Japan and U.S. HCV prototype and related variant isolates and may be suitable for detecting HCV-C9 and related isotypes as well.

Probes for detecting Japan, U.S., and C9 HCV prototypes and related variants are exemplified by KY67 (SEQ ID NO. 10), KY78 (SEQ ID NO. 18), KY81 (SEQ ID NO. 11), KY86 (SEQ ID NO. 13), KY95 (SEQ ID NO. 20), KY150 (SEQ ID NO. 42), and KY145 (SEQ ID NO. 19). Probes for detecting Japan and U.S. HCV prototype and related variants which probes do not detect the HCV-C9 prototype include KY83 (SEQ ID NO. 7), KY87 (SEQ ID NO. 14), KY84 (SEQ ID NO. 8), KY88 (SEQ ID NO. 12), KY85 (SEQ ID NO. 9), KY100 (SEQ ID NO. 21), KY148 (SEQ ID NO. 17), and KY149 (SEQ ID NO. 16). Probes KY65 (SEQ ID NO. 1), KY68 (SEQ ID NO. 26), KY82 (SEQ ID NO. 27), KY99 (SEQ ID NO. 25), KY109 (SEQ ID NO. 23), KY111 (SEQ ID NO. 24), KY80 (SEQ ID NO. 5), KY144 (SEQ ID NO. 6), and KY153 (SEQ ID NO. 15) are suitable for detecting Japan and U.S. HCV prototype and related variant isolates and may be suitable for detecting HCV-C9 and related variants as well.

Example 6

Homogeneous RT/PCR amplification of HCV RNA in the presence of UNG is a preferred method. The homogeneous RT-PCR amplification method described in Example 1 was modified to include a sterilization step. The protocol described below demonstrates that the RT and PCR reactions incorporate dUTP. Sterilization occurs at 50°C prior to the RT step. At the elevated RT-PCR reaction temperatures, UNG is inactive, and the dU containing products are not degraded. Two units of UNG (Perkin Elmer) successfully sterilized a carryover equivalent to 0.25 µl of a 100 µl amplification made with 10,000 copies of HCV RNA. Higher amounts of UNG, for example, up to 6 units per 100 µl reaction, are also suitable.

Reaction mix components were added in the following order:

	µl/Rx
50% Glycerol	16.00
10X RT Rxn. Buffer (100 mM Tris-HCl (pH 8.3), 900 mM KCl)	10.00
dGTP(10 mM); 200 µM final	2.00
dATP (10 mM); 200 µM final	2.00
dUTP (20 mM); 200 µM final	1.00
dCTP (10 mM); 200 µM final	2.00
KY80 (SEQ ID NO. 5) at 15 µM (15 pmoles each/rxn final); (+) biotinylated strand primer	1.00
KY78 (SEQ ID NO. 18) at 15 µM (15 pmoles each/rxn final); biotinyl. (-) strand, RT primer	1.00
UNG: 1 unit/µl	2.00
rTth DNA polymerase: 2.5 U/µl in 1X enzyme storage buffer*	4.00
$MnCl_2$ (10 mM); 0.9 mM final	9.00
Master Mix per tube	50.00
RNA (with carrier background** in H_2O)	50.00
total volume of reaction	100.00

*1X enzyme storage buffer = (20 mM Tris-HCl [pH 7.5], 100 mM KCl, 0.1 mM EDTA, 1mM DTT, 0.5% Tween™ 20 [Pierce Surfactamps], 50% glycerol [v/v]).

** 1 mg poly rA homopolymeric RNA from Pharmacia (No 27-poly rA has an average $S_{20,w}$ of 8.8 (Range 6-13) or some non-specific products at the annealing temperature used at input levels of less than 200 ng per reaction. Calf thymus DNA, PBL DNA, human placental DNA, and DNA from the cell line K562 have been examined and behave similarly.

Procedure:

1. Turn on TC9600 thermocycler to preheat cover.
2. Prepare reaction mix at room temperature.
3. Place tubes into thermocycler and press "Run" to restart thermocycler.
4. Start machine at file 8.
5. Suggested thermocycle conditions:

File 1: Hold 2 min. at 50°C (UNG sterilization step)
File 2: Hold 15 min. at 70°C (reverse transcription step)
File 3: Hold 1 min. at 95°C
File 4: Two Temp. PCR 15 sec. at 95°C and 10-30 sec. at 60°C for 2 cycles
File 5: Two Temp. PCR 15 sec. at 90°C and 10-30 sec. at 60°C for 38 cycles
File 6: Hold 72°C for 1 hour
File 7: Hold 15°C indefinitely
File 8: Link Files: 1, 2, 3, 4, 5, 6, and 7

At step 5, file 2, the 15 min. reaction time can be lowered to 5 minutes without decreasing the reaction efficiency. At step 5, file 5, for high G + C templates, it may be preferable to raise the denaturation temperature to 95°C. Analysis of reaction products by microtiter plate assay format generally resulted in absorbance values greater than 0.8 for positive samples and ≤ 0.5 for negative samples.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
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(ii) TITLE OF INVENTION: Primers and Probes for Hepatitis C Detection

(iii) NUMBER OF SEQUENCES: 42

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 751,305
(B) FILING DATE: 27-AUG-1991

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAAGCTTCA CCATAGATCA CT 22

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCGACACTC CACCATAGAT CACT 24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCAAGCTTAG ATCACTCCCC TGTGAGGAAC T 31

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCAAGCTTCA CGCAGAAAGC GTCTAGCCAT 30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCAGAAAGCG TCTAGCCATG GCGT 24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACGCAGAAAG CGTCTAGCCA TGGCGT 26

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTCCAGGAC CCCCCCTCCC GGGAGAGCCA 30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTACACCG GAATTGCCAG GACGACC 27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCCGCTCAA TGCCTGGAGA T 21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGAAGCTTGC TAGCCGAGTA GT 22

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGCAAGACT GCTAGCCGAG TAGT 24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGGGTCGC GAAAGGCCTT GTGGT 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTGCTTGCG AGTGCCCCGG GAGGTCTCGT 30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACTTCCGAG CGGTCGCAAC CTCG 24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCAACACTA CTCGGCTAGC AGTCT 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAGGCCTTTC GCGACCCAAC ACTACT 26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACAAGGCCT TTCGCGACCC AACACT 26

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCGCAAGCA CCCTATCAGG CAGT 24

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACTCGCAAG CACCCTATCA GGCAGT 26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGAATTCGC AAGCACCCTA TCAGGCAGT 29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGAGGTTGCG ACCGCTCGGA AGT 23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGGTTGCGAC CGCTCGGAAG T 21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AATGCCATAG AGGGGCCAAG G 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATTGCCATAG AGGGGCCAAG G 21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGAATTCAT TGCCATAGAG GGGCCAAGGA T 31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGAATTCGC CCTCATTGCC AT 22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCCACCCCAA GCCCTCATTG CCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACTGTCTTCA CGCAGAAAGC GTCTAGCCAT GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA 60

GGCCCCCCCC TCCCGGGAGA GCCATAGTGG TCTGCGGAAC CGGTGAGTAC ACCGGAATTA 120

CCGGAAAGAC TGGGTCCTTT CTTGGATAAA CCCACTCTGT GTCCGGTCAT TTGGGCGTGC 180

CCCCGCAAGA CTGCTAGCCG AGTAGCGTTG GGTTGCGAAA GGCCTTGTGG TACTGCCTGA 240

TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GCATCATGAG CACAAATCCT 300

AAACCTCAAA GAAAAACCAA AAGAAACACA AACCGCCGCC CACAGGACGT TAAGTTTCCG 360

GGTGGCGGCC AGATCGTTGG CGGAGTTTAC TTGCTGCCGC GCAGGGGCCC CAGGTTGGGT 420

GTGCGCGCGA CAAGAAAGAC TTCCGAGCGA TCCCAGCCGC GTGGGAGACG CCAGCCCATC 480

CCAAAAGATC GGCGCTCCAC CGGCAAGTCC TGGGGAAAGC CAGGAT 526

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA GCCATAGTGG 60

TCTGCGGAAC CGGTGAGTAC GCCGAATTAC CGGAAAGACT GGGTCCTTTC TTGGATAAAC 120

CCACTCTATG TCCGGTCATT TGGGCGTCCC CCGCAAGACT GCTAGCCGAG TAGCGTTGGG 180

TTGCGAAAGG CCTTGTGGTA CTGCCTGATA GGGTGCTTGC GAGTGCCCCG GGAGGTCTCG 240

TAGACCGTGC ATCATGAGCA CAGATCCTAA ACCTCAAAGA AAAACCAAAA GAAATACAAA 300

CCGCCGCCCA CAGGACGTCA AGTTCCCGGG TGGCGGCCAG ATCGTTGGCG GAGTTTACTT 360

GCTGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCACAACA AGGAAGACTT CCGAGCGATC 420

CCAGCCGCGT GGAAGACGCC AGCCCATCCC GAAAGATCGG CGCTCCACCG GTAAGTCCTG 480

GGGAAAGCCA GGAT 494

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA GCCATAGTGG 60

TCTGCGGAAC CGGTGAGTAC GCCGAATTGC CGGAAAGACT GGGTCCTTTC TTGGATAAAC 120

CCACTCTATG TCCGGTCATT TGGGCGTCCC CCGCAAGACT GCTAGCCGAG TAGCGTTGGG 180

TTGCGAAAGG CCTTGTGGTA CTGCCTGATA GGGTGCTTGC GAGTGCCCAG GGAGGTCTCG 240

TAGACCGTGC ATCATGAGCA CAAATCCTAA ACCCCAAAGA AAAACCAAAA GAAACACAAA 300

CCGCCGCCCA CAGGACGTTA AGTTCCCGGG TGGCGGCCAG ATCGTTGGCG GAGTTTACTT 360

GATGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCGCGACG AGGAAGACTT CCGAGCGATC 420

CCAGCCGCGT GGGAGACGCC AGCCCATCCC GAAAGATCGG CGTTCCACCG GCAAGTCCTG 480

GGGAAAGCCA GGAT 494

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA GCCATAGTGG 60

TCTGCGGAAC CGGTGAGTAC GCCGAATTGC CGGAAAGACT GGGTCCTTTC TTGGATTAAC 120

CCACTCTATG TCCGGTCATT TGGGCGTCCC CCGCAAGACT GCTAGCCTAG TAGCGTTGGG 180

TTGCGAACGG CCTTGTGGTA CTGCCTGATA GGGTGCTTGC GAGTGCCCCG GGAGGTCTCG 240

TAGACCGTGC ATCATGAGCA CAAATCCTAA ACCTCAAAGA AAAACCAAAA GAAACACAAA 300

CCGCCGCCCA CAGGACGTCA AGTTCCCGGG AGGCGGTCAG ATCGTTGGCG GAGTTTACTT 360

GCTGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCGCGACA AGGAAGACTT CCGAGCGATC 420

CCAGCCGCGT GGGAGACGCC AGCCCATCCC GAAAGATCGG CGCTCCACCG GCAAGTCCTG 480

GGGAAAGCCA GGAT 494

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCGTTAGTA TGAGTGTCGT ACAGCCTCCA GGCCCCCCCC TCCCGGGAGA GCCATAGTGG 60

TCTGCGGAAC CGGTGAGTAC ACCGAATTAC CGGAAAGACT GGGTCCTTTC TTGGATAAAC 120

CCACTCTATG TCCGGTCATT TGGGCGTCCC CCGCAAGACT GCTAGCCTAG TAGCGTTGGG 180

TTGCGAACGG CCTTGTGGTA CTGCCTGATA GGGTGCTTGC GAGTGCCCCG GGAGGTCTCG 240

TAGACCGTGC ATCATGAGCA CAAATCCTAA ACCTCAAAGA AAAACCAAAA GAAACACAAA 300

CCGCCGCCCA CAGGACGTCA AGTTCCCGGG TGGCGGCCAG ATCGTTGGCG GAGTTTACTT 360

GCTGCCGCGC AGGGGCCCCA GGTTGGGTGT GCGCGCGACA AGGAAGACTT CCGAACGGTC 420

CCAGCCGCGT GGGAGGCGCC AGCCCATCCC AAAAGATCGG CGCTCCACCG GCAAGTCCTG 480

GGGAAAGCCA GGAT 494

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTGCCGGAAA GACTGGGTCC TTTC 24

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAAAGAAAC ACAAACCGCC GCCC 24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGCCCATC CCGAAAGATC GGCG 24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TGTCCGGTCA TTTGGGCG 18

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAACCCACTC TATGTCCGGT C 21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTACGCCGGA ATTGCCGGAA A 21

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTCAAAGAA AAACCAAAAG A 21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGGCGTCTCC CACGCGGCTG G 21

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTTCCCCAG GACCTGCCGG T 21

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CATAGTGGTC TGCGGAACCG GTGAGT 26

Claims

1. An oligonucleotide probe for detecting hepatitis C virus nucleic acid from a Japan or US prototype strain, wherein said probe consists of a nucleic acid sequence at least 14 nucleotides in length contained in a region of HCV genomic nucleic acid corresponding to SEQ ID NO. 28 and which nucleic acid sequence is specific to said Japan and US prototype strains and is not specific to a C9 prototype strain, wherein said probe is preferably labeled.

2. The oligonucleotide probe of claim 1, wherein said probe is:

   (a) selected from the group of oligonucleotide probes consisting of KY65 (SEQ ID NO. 1), KY68 (SEQ ID NO. 26), KY82 (SEQ ID NO. 27), KY99 (SEQ ID NO. 25), KY109 (SEQ ID NO. 23), KY111 (SEQ ID NO. 24), KY80 (SEQ ID NO. 5), KY144 (SEQ ID NO. 6), and KY153 (SEQ ID NO. 15) and the oligonucleotide probes with a complementary sequences thereto; or
   (b) selected from the group of oligonucleotide probes consisting of KY83 (SEQ ID NO. 7), KY87 (SEQ ID NO. 14), KY84 (SEQ ID NO. 8), KY88 (SEQ ID NO. 12), KY85 (SEQ ID NO. 9), KY100 (SEQ ID NO. 21), KY148 (SEQ ID NO. 17) and KY149 (SEQ ID NO. 16) and the oligonucleotide probes with a complementary sequences thereto.

3. An oligonucleotide probe for detecting hepatitis C virus nucleic acid, wherein said probe consists of a nucleic acid sequence at least 14 nucleotides in length contained in a sequence selected from the group consisting of SEQ ID NO. 28, SEQ ID NO. 29, SEQ ID NO.30, SEQ ID NO. 31 and SEQ ID NO. 32, and the complement thereof, wherein said nucleic acid sequence is specific to Japan, US and C9 prototype strains.

4. The oligonucleotide probe of claim 3, wherein said probe is selected from the group of oligonucleotide probes consisting of KY67 (SEQ ID NO. 10), KY78 (SEQ ID NO. 18), KY81 (SEQ ID NO. 11), KY86 (SEQ ID NO. 13), KY95 (SEQ ID NO. 20), and KY145 (SEQ ID NO. 19) and the oligonucleotide probes with a complementary sequences thereto.

5. An oligonucleotide primer for amplifying an HCV nucleic acid wherein said primer is:

   (a) capable of amplifying a nucleic acid subsequence from an HCV strain selected from the group consisting of Japan, US and C9 prototype strains, characterized in that said primer is selected from the group consisting of KY67 (SEQ ID NO. 10), KY78 (SEQ ID NO. 18), KY80 (SEQ ID NO. 5), KY81 (SEQ ID NO. 11), KY83 (SEQ ID NO. 7), KY86 (SEQ ID NO. 13), KY88 (SEQ ID NO. 12), KY95 (SEQ ID NO. 20), KY100 (SEQ ID NO. 21), KY144 (SEQ ID NO. 6), KY145 (SEQ ID NO. 19), and KY153 (SEQ ID NO. 15); or
   (b) capable of amplifying a nucleic acid subsequence from an HCV strain selected from the group consisting of Japan and U.S. HCV prototype strains, characterized in that said primer is selected from the group consisting of KY65 (SEQ ID NO. 1), KY68 (SEQ ID NO. 26), KY98 (SEQ ID NO. 3), KY99 (SEQ ID NO. 25), KY109 (SEQ ID NO. 23), KY111 (SEQ ID NO. 24) and KY149 (SEQ ID NO. 16); or
   (c) capable of amplifying a nucleic acid subsequence from an HCV strain selected from the group consisting of Japan and US HCV prototype strains and does not amplify HCV-C9 prototype virus nucleic acids, characterized in that said primer is selected from the group consisting of KY84 (SEQ ID NO. 8), KY85 (SEQ ID NO. 9), KY87 (SEQ ID NO. 14), and KY148 (SEQ ID NO. 17), whereby said primer is preferably labeled.

6. An oligonucleotide probe or primer selected from the group consisting of:

   KY96 SEQ ID NO: 4 5'-CCAAGCTTCACGCAGAAAGCGTCTAGCCAT
   KY79 SEQ ID NO: 2 5'-GGCGACACTCCACCATAGATCACT; and
   KY110 SEQ ID NO: 225'-AGGTTGCGACCGCTCGGAAGT,

   which oligonucleotide probe or primer is preferably labeled.

7. A process for detecting a nucleic acid from a hepatitis C virus, characterized in that an oligonucleotide probe as claimed in any one of claims 1 to 4 or 6 is used as a probe.

8. The process of claim 7, which further comprises an amplification step, in which a subsequence of the hepatitis C virus genome is first amplified, whereby said amplification is preferably achieved by the use the polymerase chain reaction method.

9. A process for amplifying nucleic acid from a hepatitis C virus, characterized in that an oligonucleotide primer of claim 5 or 6 is used.

10. A process for detecting a nucleic acid from a hepatitis C virus, characterized in that an oligonucleotide selected from the group of:

KY84 SEQ ID NO: 8 5'-GAGTACACCGGAATTGCCAGGACGACC
KY85 SEQ ID NO: 9 5'-ACCCGCTCAATGCCTGGAGAT
KY88 SEQ ID NO: 125'-GTTGGGTCGCGAAAGGCCTTGTGGT

is used as a probe and wherein a subsequence of the hepatitis C nucleic acid in the sample is first amplified using the primer pair:

KY80 SEQ ID NO: 5 5'-GCAGAAAGCGTCTAGCCATGGCGT and
KY78 SEQ ID NO: 185'-CTCGCAAGCACCCTATCAGGCAGT.

11. A kit for detecting the presence of a nucleic acid from a hepatitis C virus, the kit comprising a compartment which contains a oligonucleotide probe as claimed in any one of claims 1 to 4 or 6.

12. A kit for amplifying a nucleic acid from a hepatitis C virus, the kit comprising a compartment which contains an oligonucleotide primer as claimed in claim 5 or claim 6 and one or more reverse-transcription or amplification reagents, optionally further comprising one or more oligonucleotide probes as claimed in any one of claims 1 to 4 or 6.

13. Use of an oligonucleotide probe as claimed in any one of claims 1 to 4 or 6 for detecting the presence of hepatitis C genomic nucleic acid from an HCV strain.

14. Use of an oligonucleotide primer as claimed in claim 5 or claim 6 for amplifying a 5'-terminal region of the genome of an HCV strain.

Figure 1

A.

Alignment of 5' Untranslated Region and Contiguous Open Reading Frame of C9 Variant With Additional Isolates Prototype HCV Sequences

```
Seq. ID Nos.
(Seq. ID No. 29) C  9  5'----------A----------C----------
(Seq. ID No. 30) R116              ----------A----------C----------
(Seq. ID No. 31) R45               ----------A----------C----------
(Seq. ID No. 32) R110              ----------A----------C----------
(Seq. ID No. 33) R43               ----------A----------C----------
                 HCV-J1  ----------
                 HCV-J4  ----------
                 HCV-J   ----------T----------
                 HCV-BK  ----------
           HCV-1 US-PT   ACTGTCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCTCCCGGGAGAGCCATAGTG
                         45

C9          ----------A--G-A-A---T----------A-----A---TG--T-C--TC----------
R116        ----------G--- ----A--G-A-A---T----------A-----A---T---T-C--TC---------- ------
R45         ----------G--- -------G-A-A---T----------A-----A---T---T-C--TC---------- ------
R110        ----------G--- -------G-A-A---T----------T-----A---T---T-C--TC---------- ------
R43         ---------- ----A--G-A-A---T----------A-----A---T---T-C--TC---------- ------
HCV-J1      ----------A----------C-------
HCV-J4      ----------
HCV-J       ----------
HCV-BK      ----------
HCV-1 US-PT GTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCG
            134

C9          ----------C-------T----------
R116        ----------C-------T----------T-
R45         ----------C-------T----------A----------T-
R110        ----------T-----C-------T-----C----------T-
R43         ----------T-----C-------T-----C----------T-
HCV-J1      ----------
HCV-J4      -G----------
HCV-J       -G----------T-
HCV-BK      -G----------
HCV-1 US-PT CAAGACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACC
            230
```

B.

```
C9-2 PT      --------A----------------G-----C----A-A-----A-----C--------------T-----T----------C------
R116         --------AG---------------G-----C----A-A--T--A-----C--------------------------------C------
R45          --------A----------C----G-----C----A-A-----A-----C--------------T----------------C------
R110         --------A----------------G-----C----A-A-----A-----C--------------------------A-----------
R43          --------A----------------G-----C----A-A-----A-----C--------------------------------C------
HCV-J1       ----------T---C----------G-----C-------------------------------------------------------
HCV-J4       -------------------------G-----C-----------------C--------------------------C--T---------
HCV-J        --------A----------------G-----C-----------------C--------------T----------C--T---------
HCV-BK       -------------------------G-----C-----------------C--------------------------C--T---------
HCV-1 US-PT ATGAGCACGAATCCTAAACCTCAAAAAAAAAAACAAACGTAACACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATC
            330

C9-2 PT      -----C------------C----------------C--G----------------A----------------A--C--G--G--T--G
R116         -----C------------C----------------C--G------------A-A--A--G--------------A--C--G--G--T--A
R45          -----C------------A----------------C--G--------------------G--------------A--C--G--G--T--G
R110         -----C------------C----------------C--G----------------A--G--------------A--C--G--G--T--G
R43          -----C------------C----------------C--G----------------A--G----------A-----C--G--G--T--G
HCV-J1       ------------------------------------------------------------G-----------------------------
HCV-J4       ----------------C-------------------C--G----------------T--G-------------------------T--A
HCV-J        ----------------C-------------------C--G----------------T--G-------------------------T--A
HCV-BK       ----------------C-------------------C--G--------------C-C--G-------------------------T--A
HCV-1 US-PT GTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGT
            420

C9-2 PT      -----C-----C-----A--A-A---G--CT--ACC------T------GAA----A--A- 3'
R116         -----C-----C-----G--A-A---G--CT--ACC--T---T------GAA----A--A-
R45          -----C-----C-----G--A-A---G--TT--ACC------T------GAA----A--A-
R110         -----C-----C-----G--A-A---G--CT--ACC------T------GAA----A--A-
R43          --G--C-----C-----A--A-A---G--CT--ACC------T------GAA----A--A-
HCV-J1       ----------------------TG-------------------------------------
HCV-J4       T-G--A--A----------------C--A-----------G--------------------
HCV-J        --G--A--A----------------C-----------T----------------------
HCV-BK       --G--A--A----------------C----------------------------------
HCV-1 US-PT AGACGTCAGCCTATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGT
            510                                                      570
```